

# Sequence Table

Sequence No. 1

Length of sequence: 4228

Type of sequence: Nucleic acid

## Sequence

ATG TTC CCC ACC GAG AGC GCA TGG CTT GGG AAG CGA GGC GCG AAC CCG	48
Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro	
-35 -30 -25	
GGC CCC GAA GCT GCA CTC CGG GAG ACG GTG ATG CTG TTG CTG-TGC CTG	96
Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu	
-20 -15 -10	
GGG GTC CCG ACC GGC AGG CCT TAC AAC GTG GAC ACT GAG AGC GCG CTG	144
Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu	
-5 1 5	
CTT TAC CAG GGC CCC CAC AAC ACG CTG TTC GGC TAC TCG GTC GTG CTG	192
Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu	
10 15 20 25	
CAC AGC CAC GGG GCG AAC CGA TGG CTC CTA GTG GGT GCG CCC ACT GCC	240
His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala	
30 35 40	
AAC TGG CTC GCC AAC GCT TCA GTG ATC AAT CCC GGG GCG ATT TAC AGA	288
Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg	
45 50 55	
TGC AGG ATC GGA AAG AAT CCC GGC CAG ACG TGC GAA CAG CTC CAG CTG	336
Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu	
60 65 70	
GGT AGC CCT AAT GGA GAA CCT TGT GGA AAG ACT TGT TTG GAA GAG AGA	384
Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg	
75 80 85	

GAC AAT CAG TGG TTG GGG GTC ACA CTT TCC AGA CAG CCA GGA GAA AAT	432
Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn	
90 95 100 105	
GGA TCC ATC GTG ACT TGT GGG CAT AGA TGG AAA AAT ATA TTT TAC ATA	480
Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile	
110 115 120	
AAG AAT GAA AAT AAG CTC CCC ACT GGT GGT TGC TAT GGA GTG CCC CCT	528
Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro	
125 130 135	
GAT TTA CGA ACA GAA CTG AGT AAA AGA ATA GCT CCG TGT TAT CAA GAT	576
Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp	
140 145 150	
TAT GTG AAA AAA TTT GGA GAA AAT TTT GCA TCA TGT CAA GCT GGA ATA	624
Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile	
155 160 165	
TCC AGT TTT TAC ACA AAG GAT TTA ATT GTG ATG GGG GCC CCA GGA TCA	672
Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser	
170 175 180 185	
TCT TAC TGG ACT GGC TCT CTT TTT GTC TAC AAT ATA ACT ACA AAT AAA	720
Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys	
190 195 200	
TAC AAG GCT TTT TTA GAC AAA CAA AAT CAA GTA AAA TTT GGA AGT TAT	768
Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr	
205 210 215	
TTA GGA TAT TCA GTC GGA GCT GGT CAT TTT CGG AGC CAG CAT ACT ACC	816
Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr	
220 225 230	
GAA GTA GTC GGA GGA GCT CCT CAA CAT GAG CAG ATT GGT AAG GCA TAT	864
Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr	
235 240 245	



AAT GGC TAT GTA GAT GTA GCA GTT GGT GCT TTT CGG TCT GAT TCT GCT	1392
Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala	
410                      415                      420                      425	
GTC TTG CTA AGG ACA AGA CCT GTA GTA ATT GTT GAC GCT TCT TTA AGC	1440
Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser	
430                      435                      440	
CAC CCT GAG TCA GTA AAT AGA ACG AAA TTT GAC TGT GTT GAA AAT GGA	1488
His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly	
445                      450                      455	
TGG CCT TCT GTG TGC ATA GAT CTA ACA CTT TGT TTC TCA TAT AAG GGC	1536
Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly	
460                      465                      470	
AAG GAA GTT CCA GGT TAC ATT GTT TTG TTT TAT AAC ATG AGT TTG GAT	1584
Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp	
475                      480                      485	
GTG AAC AGA AAG GCA GAG TCT CCA CCA AGA TTC TAT TTC TCT TCT AAT	1632
Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn	
490                      495                      500                      505	
GGA ACT TCT GAC GTG ATT ACA GGA AGC ATA CAG GTG TCC AGC AGA GAA	1680
Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu	
510                      515                      520	
GCT AAC TGT AGA ACA CAT CAA GCA TTT ATG CGG AAA GAT GTG CGG GAC	1728
Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp	
525                      530                      535	
ATC CTC ACC CCA ATT CAG ATT GAA GCT GCT TAC CAC CTT GGT CCT CAT	1776
Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His	
540                      545                      550	
GTC ATC AGT AAA CGA AGT ACA GAG GAA TTC CCA CCA CTT CAG CCA ATT	1824
Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile	
555                      560                      565	

CTT CAG CAG AAG AAA GAA AAA GAC ATA ATG AAA AAA ACA ATA AAC TTT	1872
Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe	
570                      575                      580                      585	
GCA AGG TTT TGT GCC CAT GAA AAT TGT TCT GCT GAT TTA CAG GTT TCT	1920
Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser	
590                      595                      600	
GCA AAG ATT GGG TTT TTG AAG CCC CAT GAA AAT AAA ACA TAT CTT GCT	1968
Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala	
605                      610                      615	
GTT GGG AGT ATG AAG ACA TTG ATG TTG AAT GTG TCC TTG TTT AAT GCT	2016
Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala	
620                      625                      630	
GGA GAT GAT GCA TAT GAA ACG ACT CTA CAT GTC AAA CTA CCC GTG GGT	2064
Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly	
635                      640                      645	
CTT TAT TTC ATT AAG ATT TTA GAG CTG GAA GAG AAG CAA ATA AAC TGT	2112
Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Glu Lys Gln Ile Asn Cys	
650                      655                      660                      665	
GAA GTC ACA GAT AAC TCT GGC GTG GTA CAA CTT GAC TGC AGT ATT GGC	2160
Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly	
670                      675                      680	
TAT ATA TAT GTA GAT CAT CTC TCA AGG ATA GAT ATT AGC TTT CTC CTG	2208
Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu	
685                      690                      695	
GAT GTG AGC TCA CTC AGC AGA GCG GAA GAG GAC CTC AGT ATC ACA GTG	2256
Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val	
700                      705                      710	
CAT GCT ACC TGT GAA AAT GAA GAG GAA ATG GAC AAT CTA AAG CAC AGC	2304
His Ala Thr Cys Glu Asn Glu Glu Glu Met Asp Asn Leu Lys His Ser	
715                      720                      725	

AGA GTG ACT GTA GCA ATA CCT TTA AAA TAT GAG GTT AAG CTG ACT GTT	2352
Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val	
730                                      735                                      740                                      745	
CAT GGG TTT GTA AAC CCA ACT TCA TTT GTG TAT GGA TCA AAT GAT GAA	2400
His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu	
750                                      755                                      760	
AAT GAG CCT GAA ACG TGC ATG GTG GAG AAA ATG AAC TTA ACT TTC CAT	2448
Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His	
765                                      770                                      775	
GTT ATC AAC ACT GGC AAT AGT ATG GCT CCC AAT GTT AGT GTG GAA ATA	2496
Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile	
780                                      785                                      790	
ATG GTA CCA AAT TCT TTT AGC CCC CAA ACT GAT AAG CTG TTC AAC ATT	2588
Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile	
795                                      800                                      805	
TTG GAT GTC CAG ACT ACT ACT GGA GAA TGC CAC TTT GAA AAT TAT CAA	2592
Leu Asp Val Gln Thr Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln	
810                                      815                                      820                                      825	
AGA GTG TGT GCA TTA GAG CAG CAA AAG AGT GCA ATG CAG ACC TTG AAA	2640
Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys	
830                                      835                                      840	
GGC ATA GTC CGG TTC TTG TCC AAG ACT GAT AAG AGG CTA TTG TAC TGC	2688
Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys	
845                                      850                                      855	
ATA AAA GCT GAT CCA CAT TGT TTA AAT TTC TTG TGT AAT TTT GGG AAA	2736
Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys	
860                                      865                                      870	
ATG GAA AGT GGA AAA GAA GCC AGT GTT CAT ATC CAA CTG GAA GGC CGG	2784
Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg	
875                                      880                                      885	



ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC 3589  
 Met. Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 985 990 995  
 CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG 3637  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 1000 1005 1010 1015  
 GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG 3685  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 1020 1025 1030  
 TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT 3733  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 1035 1040 1045  
 GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC 3781  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 1050 1055 1060  
 ATC GAG AAA ACC ATC TCC AAA GCC AAA GGTGGGACCC GTGGGGTGCG 3828  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys  
 1065 1070  
 AGGGCCACAT GGACAGAGGC CGGCTCGGCC CACCCTCTGC CCTGAGAGTG ACCGCTGTAC 3888  
 CAACCTCTGT CCTACA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG 3937  
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 1075 1080  
 CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC 3985  
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
 1085 1090 1095  
 CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC 4033  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 1100 1105 1110 1115



AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACC CCT CCC GTG CTG GAT	4081
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp	
1120 1125 1130	
TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC	4129
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser	
1135 1140 1145	
AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT	4177
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala	
1150 1155 1160	
CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA	4225
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
1165 1170 1175	
TGA	4228

Sequence No. 2

Length of sequence: 3463

Type of sequence: Nucleic acid

Sequence

ATG AAT TTA CAA CCA ATT TTC TGG ATT GGA CTG ATC AGT TCA GTT TGC	48
Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys	
-20 -15 -10 -5	
TGT GTG TTT GCT CAA ACA GAT GAA AAT AGA TGT TTA AAA GCA AAT GCC	96
Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala	
1 5 10	
AAA TCA TGT GGA GAA TGT ATA CAA GCA GGG CCA AAT TGT GGG TGG TGC	144
Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys	
15 20 25	
ACA AAT TCA ACA TTT TTA CAG GAA GGA ATG CCT ACT TCT GCA CGA TGT	192
Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys	
30 35 40	

GAT GAT TTA GAA GCC TTA AAA AAG AAG GGT TGC CCT CCA GAT GAC ATA	240
Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile	
45 50 55 60	
GAA AAT CCC AGA GGC TCC AAA GAT ATA AAG AAA AAT AAA AAT GTA ACC	288
Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr	
65 70 75	
AAC CGT AGC AAA GGA ACA GCA GAG AAG CTC AAG CCA GAG GAT ATT CAT	336
Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His	
80 85 90	
CAG ATC CAA CCA CAG CAG TTG GTT TTG CGA TTA AGA TCA GGG GAG CCA	384
Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro	
95 100 105	
CAG ACA TTT ACA TTA AAA TTC AAG AGA GCT GAA GAC TAT CCC ATT GAC	432
Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp	
110 115 120	
CTC TAC TAC CTT ATG GAC CTG TCT TAT TCA ATG AAA GAC GAT TTG GAG	480
Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu	
125 130 135 140	
AAT GTA AAA AGT CTT GGA ACA GAT CTG ATG AAT GAA ATG AGG AGG ATT	528
Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile	
145 150 155	
ACT TCG GAC TTC AGA ATT GGA TTT GGC TCA TTT GTG GAA AAG ACT GTG	576
Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val	
160 165 170	
ATG CCT TAC ATT AGC ACA ACA CCA GCT AAG CTC AGG AAC CCT TGC ACA	624
Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr	
175 180 185	
AGT GAA CAG AAC TGC ACC ACC CCA TTT AGC TAC AAA AAT GTG CTC ACT	672
Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser	
190 195 200	

CTT	ACT	AAT	AAA	GGA	GAA	GTA	TTT	AAT	GAA	CTT	GTT	GGA	AAA	CAG	CGC	720
Leu	Thr	Asn	Lys	Gly	Glu	Val	Phe	Asn	Glu	Leu	Val	Gly	Lys	Gln	Arg	
205				210						215					220	
ATA	TCT	GGA	AAT	TTG	GAT	TCT	CCA	GAA	GGT	GGT	TTC	GAT	GCC	ATC	ATG	768
Ile	Ser	Gly	Asn	Leu	Asp	Ser	Pro	Glu	Gly	Gly	Phe	Asp	Ala	Ile	Met	
				225						230					235	
CAA	GTT	GCA	GTT	TGT	GGA	TCA	CTG	ATT	GGC	TGG	AGG	AAT	GTT	ACA	CGG	816
Gln	Val	Ala	Val	Cys	Gly	Ser	Leu	Ile	Gly	Trp	Arg	Asn	Val	Thr	Arg	
				240						245					250	
CTG	CTG	GTG	TTT	TCC	ACA	GAT	GCC	GGG	TTT	CAC	TTT	GCT	GGA	GAT	GGG	864
Leu	Leu	Val	Phe	Ser	Thr	Asp	Ala	Gly	Phe	His	Phe	Ala	Gly	Asp	Gly	
				255						260					265	
AAA	CTT	GGT	GGC	ATT	GTT	TTA	CCA	AAT	GAT	GGA	CAA	TGT	CAC	CTG	GAA	912
Lys	Leu	Gly	Gly	Ile	Val	Leu	Pro	Asn	Asp	Gly	Gln	Cys	His	Leu	Glu	
				270						275					280	
AAT	AAT	ATG	TAC	ACA	ATG	AGC	CAT	TAT	TAT	GAT	TAT	CCT	TCT	ATT	GCT	960
Asn	Asn	Met	Tyr	Thr	Met	Ser	His	Tyr	Tyr	Asp	Tyr	Pro	Ser	Ile	Ala	
285				290						295					300	
CAC	CTT	GTC	CAG	AAA	CTG	AGT	GAA	AAT	AAT	ATT	CAG	ACA	ATT	TTT	GCA	1008
His	Leu	Val	Gln	Lys	Leu	Ser	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Phe	Ala	
				305						310					315	
GTT	ACT	GAA	GAA	TTT	CAG	CCT	GTT	TAC	AAG	GAG	CTG	AAA	AAC	TTG	ATC	1056
Val	Thr	Glu	Glu	Phe	Gln	Pro	Val	Tyr	Lys	Glu	Leu	Lys	Asn	Leu	Ile	
				320						325					330	
CCT	AAG	TCA	GCA	GTA	GGA	ACA	TTA	TCT	GCA	AAT	TCT	AGC	AAT	GTA	ATT	1104
Pro	Lys	Ser	Ala	Val	Gly	Thr	Leu	Ser	Ala	Asn	Ser	Ser	Asn	Val	Ile	
				335						340					345	
CAG	TTG	ATC	ATT	GAT	GCA	TAC	AAT	TCC	CTT	TCC	TCA	GAA	GTC	ATT	TTG	1152
Gln	Leu	Ile	Ile	Asp	Ala	Tyr	Asn	Ser	Leu	Ser	Ser	Glu	Val	Ile	Leu	
350				355						360						





TAT TCA GTG AAT GGG AAC AAC GAG GTC ATG GTT CAT GTT GTG GAG AAT	2160
Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn	
685                      690                      695                      700	
CCA GAG TGT CCC ACT GGT CCA GAG GAT CCC GAG CTGCTGGAAG CAGGCTCAGC	2213
Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu	
705                      710	
GCTCCTGCCT GGACGCATCC CGGCTATGCA GCCCCAGTCC AGGGCAGCAA GGCAGGCCCC	2273
GTCTGCCTCT TCACCCGGAG CCTCTGCCCC CCCCACATCAT GCTCAGGGAG AGGGTCTTCT	2333
GGCTTTTTTCC CAGGCTCTGG GCAGGCACAG GCTAGGTGCC CCTAACCCAG GCCCTGCACA	2393
CAAAGGGGCA GGTGCTGGGC TCAGACCTGC CAAGAGCCAT ATCCGGGAGG ACCCTGCCCC	2453
TGACCTAAGC CCACCCCAAA GGCCAAACTC TCCACTCCCT CAGCTCGGAC ACCTTCTCTC	2513
CTCCCAGATT CCAGTAACTC CCAATCTTCT CTCTGCA GAG CCC AAA TCT TGT GAC	2568
Glu Pro Lys Ser Cys Asp	
715	
AAA ACT CAC ACA TGC CCA CCG TGC CCA GGTAAGCCAG CCCAGGCCTC	2615
Lys Thr His Thr Cys Pro Pro Cys Pro	
720                      725	
GCCCTCCAGC TCAAGGCGGG ACAGGTGCCC TAGAGTAGCC TGCATCCAGG GACAGGCCCC	2675
AGCCGGGTGC TGACACGTCC ACCTCCATCT CTTCCTCA GCA CCT GAA CTC CTG	2728
Ala Pro Glu Leu Leu	
730	
GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC	2776
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
735                      740                      745	
ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC	2824
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
750                      755                      760	
CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG	2872
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
765                      770                      775	

GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG	2920
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
780 785 790 795	
TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT	2968
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
800 805 810	
GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC	3016
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
815 820 825	
ATC GAG AAA ACC ATC TCC AAA GCC AAA GGTGGGACCC GTGGGGTGCG	3063
Ile Glu Lys Thr Ile Ser Lys Ala Lys	
830 835	
AGGGCCACAT GGACAGAGGC CGGCTCGGCC CACCCTCTGC CCTGAGAGTG ACCGCTGTAC	3123
CAACCTCTGT CCTACA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG	3172
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu	
840 845	
CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC	3220
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys	
850 855 860	
CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC	3268
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser	
865 870 875	
AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAT	3316
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp	
880 885 890 895	
TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC	3364
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser	
900 905 910	

AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT 3412  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
 915 920 925  
 CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA 3460  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 930 935 940  
 TGA 3463

Sequence No. 3

Length of sequence: 13

Type of sequence: Amino acid

Topology: Linear

Kind of sequence: Peptide

Sequence

Cys Leu His Gly Pro Glu Ile Leu Asp Val Pro Ser Thr

1 5 10

Sequence No. 4

Length of sequence: 31

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GCGGATCCCG AGCTGCTGGA AGCAGGCTCA G

31

Sequence No. 5

Length of sequence: 27

Type of sequence: Nucleic acid

Number of strands: Single



Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

CCTCTAGACG GCCGTCGCAC TCATTTA

27

Sequence No. 6

Length of sequence: 73

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

CTAGACCACC ATGTTCCCA CCGAGAGCGC ATGGCTTGGG AAGCGAGGCG CGAACCCGGG  
CCCCGGAGCT GCA

73

Sequence No. 7

Length of sequence: 65

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GCTTCGGGGC CCGGGTTCGC GCCTCGCTTC CCAAGCCATG CGCTCTCGGT GGGGAACATG  
GTGCT

65

Sequence No. 8

Length of sequence: 51

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

CTCCGGGAGA CGGTGATGCT GTTGCTGTGC CTGGGGGTCC CGACCGGCAG G

51

Sequence No. 9

Length of sequence: 55

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Straight chain

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

CCTGCCGGTC GGGACCCCCA GGCACAGCAA CAGCATCACC GTCTCCCGGA GTCGA

55

Sequence No. 10

Length of sequence: 37

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

CACTGCAGGC AGGCCTTACA ACGTGGACAC TGAGAGC

37

Sequence No. 11

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

GCAGAAACCT GTAAATCAGC AG

22

Sequence No. 12

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

GCATTTATGC GGAAAGATGT GC

22

Sequence No. 13

Length of sequence: 29

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

CGGGATCCGT GAAATAACGT TTGGGTCTT

29

Sequence No. 14

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

GCGGAAAAGA TGAATTTACA AC

22

Sequence No. 15

Length of sequence: 27

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA

Sequence

GTGGGATCCT CTGGACCACT GGGACAC

27

Sequence No. 16

Length of sequence: 10

Type of sequence: Amino acid

Topology: Linear

Kind of sequence: Peptide

Sequence

Gly Pro Glu Ile Leu Asp Val Pro Ser Thr

1 5 10

Sequence No. 17

Length of sequence: 10

Type of sequence: Amino acid

Topology: Linear

Kind of sequence: Peptide

Sequence

Gly Pro Glu Ile Leu Glu Val Pro Ser Thr

1 5 10

Sequence No. 18

Length of sequence: 6

Type of sequence: Amino acid

Topology: Linear

Kind of sequence: Peptide

# Sequence

Gly Arg Gly Asp Ser Pro

1 5

Sequence No. 19

Length of sequence: 4675

Type of sequence: Nucleic acid

## Sequence

ATG GGG CCA GAA CGG ACA GGG GCC GCG CCG CTG CCG CTG CTG CTG GTG	48
Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val	
-25 -20 -15	
TTA GCG CTC AGT CAA GGC ATT TTA AAT TGT TGT TTG GCC TAC AAT GTT	96
Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val	
-10 -5 1	
GGT CTC CCA GAA GCA AAA ATA TTT TCC GGT CCT TCA AGT GAA CAG TTT	144
Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe	
5 10 15	
GGG TAT GCA GTG CAG CAG TTT ATA AAT CCA AAA GGC AAC TGG TTA CTG	192
Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu	
20 25 30 35	
GTT GGT TCA CCC TGG AGT GGC TTT CCT GAG AAC CGA ATG GGA GAT GTG	240
Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val	
40 45 50	
TAT AAA TGT CCT GTT GAC CTA TCC ACT GCC ACA TGT GAA AAA CTA AAT	288
Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn	
55 60 65	
TTG CAA ACT TCA ACA AGC ATT CCA AAT GTT ACT GAG ATG AAA ACC AAC	336
Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn	
70 75 80	

ATG AGC CTC GGC TTG ATC CTC ACC AGG AAC ATG GGA ACT GGA GGT TTT	384
Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe	
85 90 95	
CTC ACA TGT GGT CCT CTG TGG GCA CAG CAA TGT GGG AAT CAG TAT TAC	432
Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr	
100 105 110 115	
ACA ACG GGT GTG TGT TCT GAC ATC AGT CCT GAT TTT CAG CTC TCA GCC	480
Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala	
120 125 130	
AGC TTC TCA CCT GCA ACT CAG CCC TGC CCT TCC CTC ATA GAT GTT GTG	528
Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val	
135 140 145	
GTT GTG TGT GAT GAA TCA AAT AGT ATT TAT CCT TGG GAT GCA GTA AAG	576
Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys	
150 155 160	
AAT TTT TTG GAA AAA TTT GTA CAA GGC CTT GAT ATA GGC CCC ACA AAG	624
Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys	
165 170 175	
ACA CAG GTG GGG TTA ATT CAG TAT GCC AAT AAT CCA AGA GTT GTG TTT	672
Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe	
180 185 190 195	
AAC TTG AAC ACA TAT AAA ACC AAA GAA GAA ATG ATT GTA GCA ACA TCC	720
Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser	
200 205 210	
CAG ACA TCC CAA TAT GGT GGG GAC CTC ACA AAC ACA TTC GGA GCA ATT	768
Gln Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile	
215 220 225	
CAA TAT GCA AGA AAA TAT GCC TAT TCA GCA GCT TCT GGT GGG CGA CGA	816
Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg	
230 235 240	

AGT GCT ACG AAA GTA ATG GTA GTT GTA ACT GAC GGT GAA TCA CAT GAT	864
Ser Ala Thr Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp	
245 250 255	
GGT TCA ATG TTG AAA GCT GTG ATT GAT CAA TGC AAC CAT GAC AAT ATA	912
Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile	
260 265 270 275	
CTG AGG TTT GGC ATA GCA GTT CTT GGG TAC TTA AAC AGA AAC GCC CTT	960
Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu	
280 285 290	
GAT ACT AAA AAT TTA ATA AAA GAA ATA AAA GCG ATC GCT AGT ATT CCA	1008
Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro	
295 300 305	
ACA GAA AGA TAC TTT TTC AAT GTG TCT GAT GAA GCA GCT CTA CTA GAA	1056
Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu	
310 315 320	
AAG GCT GGG ACA TTA GGA GAA CAA ATT TTC AGC ATT GAA GGT ACT GTT	1104
Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val	
325 330 335	
CAA GGA GGA GAC AAC TTT CAG ATG GAA ATG TCA CAA GTG GGA TTC AGT	1152
Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser	
340 345 350 355	
GCA GAT TAC TCT TCT CAA AAT GAT ATT CTG ATG CTG GGT GCA GTG GGA	1200
Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly	
360 365 370	
GCT TTT GGC TGG AGT GGG ACC ATT GTC CAG AAG ACA TCT CAT GGC CAT	1248
Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His	
375 380 385	
TTG ATC TTT CCT AAA CAA GCC TTT GAC CAA ATT CTG CAG GAC AGA AAT	1296
Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn	
390 395 400	

CAC AGT TCA TAT TTA GGT TAC TCT GTG GCT GCA ATT TCT ACT GGA GAA	1344
His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu	
405 410 415	
AGC ACT CAC TTT GTT GCT GGT GCT CCT CGG GCA AAT TAT ACC GGC CAG	1392
Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln	
420 425 430 435	
ATA GTG CTA TAT AGT GTG AAT GAG AAT GGC AAT ATC ACG GTT ATT CAG	1440
Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln	
440 445 450	
GCT CAC CGA GGT GAC CAG ATT GGC TCC TAT TTT GGT AGT GTG CTG TGT	1488
Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys	
455 460 465	
TCA GTT GAT GTG GAT AAA GAC ACC ATT ACA GAC GTG CTC TTG GTA GGT	1536
Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly	
470 475 480	
GCA CCA ATG TAC ATG AGT GAC CTA AAG AAA GAG GAA GGA AGA GTC TAC	1584
Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr	
485 490 495	
CTG TTT ACT ATC AAA AAG GGC ATT TTG GGT CAG CAC CAA TTT CTT GAA	1632
Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu	
500 505 510 515	
GGC CCC GAG GGC ATT GAA AAC ACT CGA TTT GGT TCA GCA ATT GCA GCT	1680
Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala	
520 525 530	
CTT TCA GAC ATC AAC ATG GAT GGC TTT AAT GAT GTG ATT GTT GGT TCA	1728
Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser	
535 540 545	
CCA CTA GAA AAT CAG AAT TCT GGA GCT GTA TAC ATT TAC AAT GGT CAT	1776
Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His	
550 555 560	



CAG GGC ACT ATC CGC ACA AAG TAT TCC CAG AAA ATC TTG GGA TCC GAT	1824
Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp	
565 570 575	
GGA GCC TTT AGG AGC CAT CTC CAG TAC TTT GGG AGG TCC TTG GAT GGC	1872
Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly	
580 585 590 595	
TAT GGA GAT TTA AAT GGG GAT TCC ATC ACC GAT GTG TCT ATT GGT GCC	1920
Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala	
600 605 610	
TTT GGA CAA GTG GTT CAA CTC TGG TCA CAA AGT ATT GCT GAT GTA GCT	1968
Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala	
615 620 625	
ATA GAA GCT TCA TTC ACA CCA GAA AAA ATC ACT TTG GTC AAC AAG AAT	2016
Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn	
630 635 640	
GCT CAG ATA ATT CTC AAA CTC TGC TTC AGT GCA AAG TTC AGA CCT ACT	2064
Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr	
645 650 655	
AAG CAA AAC AAT CAA GTG GCC ATT GTA TAT AAC ATC ACA CTT GAT GCA	2112
Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala	
660 665 670 675	
GAT GGA TTT TCA TCC AGA GTA ACC TCC AGG GGG TTA TTT AAA GAA AAC	2160
Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn	
680 685 690	
AAT GAA AGG TGC CTG CAG AAG AAT ATG GTA GTA AAT CAA GCA CAG AGT	2208
Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser	
695 700 705	
TGC CCC GAG CAC ATC ATT TAT ATA CAG GAG CCC TCT GAT GTT GTC AAC	2256
Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn	
710 715 720	

TCT TTG GAT TTG CGT GTG GAC ATC AGT CTG GAA AAC CCT GGC ACT AGC	2304
Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser	
725 730 735	
CCT GCC CTT GAA GCC TAT TCT GAG ACT GCC AAG GTC TTC AGT ATT CCT	2352
Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro	
740 745 750 755	
TTC CAC AAA GAC TGT GGT GAG GAT GGA CTT TGC ATT TCT GAT CTA GTC	2400
Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val	
760 765 770	
CTA GAT GTC CGA CAA ATA CCA GCT GCT CAA GAA CAA CCC TTT ATT GTC	2448
Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val	
775 780 785	
AGC AAC CAA AAC AAA AGG TTA ACA TTT TCA GTA ACA CTG AAA AAT AAA	2496
Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys	
790 795 800	
AGG GAA AGT GCA TAC AAC ACT GGA ATT GTT GTT GAT TTT TCA GAA AAC	2544
Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn	
805 810 815	
TTG TTT TTT GCA TCA TTC TCC CTA CCG GTT GAT GGG ACA GAA GTA ACA	2592
Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr	
820 825 830 835	
TGC CAG GTG GCT GCA TCT CAG AAG TCT GTT GCC TGC GAT GTA GGC TAC	2640
Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr	
840 845 850	
CCT GCT TTA AAG AGA GAA CAA CAG GTG ACT TTT ACT ATT AAC TTT GAC	2688
Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp	
855 860 865	
TTC AAT CTT CAA AAC CTT CAG AAT CAG GCG TCT CTC AGT TTC CAA GCC	2736
Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala	
870 875 880	

TTA AGT GAA AGC CAA GAA GAA AAC AAG GCT GAT AAT TTG GTC AAC CTC	2784
Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu	
885 890 895	
AAA ATT CCT CTC CTG TAT GAT GCT GAA ATT CAC TTA ACA AGA TCT ACC	2832
Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr	
900 905 910 915	
AAC ATA AAT TTT TAT GAA ATC TCT TCG GAT GGG AAT GTT CCT TCA ATC	2880
Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile	
920 925 930	
GTG CAC AGT TTT GAA GAT GTT GGT CCA AAA TTC ATC TTC TCC CTG AAG	2928
Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys	
935 940 945	
GTA ACA ACA GGA AGT GTT CCA GTA AGC ATG GCA ACT GTA ATC ATC CAC	2976
Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His	
950 955 960	
ATC CCT CAG TAT ACC AAA GAA AAG AAC CCA CTG ATG TAC CTA ACT GGG	3024
Ile Pro Gln Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly	
965 970 975	
GTG CAA ACA GAC AAG GCT GGT GAC ATC AGT TGT AAT GCA GAT ATC AAT	3072
Val Gln Thr Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn	
980 985 990 995	
CCA CTG AAA ATA GGA CAA ACA TCT TCT TCT GTA TCT TTC AAA AGT GAA	3120
Pro Leu Lys Ile Gly Gln Thr Ser Ser Ser Val Ser Phe Lys Ser Glu	
1000 1005 1010	
AAT TTC AGG CAC ACC AAA GAA TTG AAC TGC AGA ACT GCT TCC TGT AGT	3168
Asn Phe Arg His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser	
1015 1020 1025	
AAT GTT ACC TGC TCG TTG AAA GAC GTT CAC ATG AAA GGA GAA TAC TTT	3216
Asn Val Thr Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe	
1030 1035 1040	

GTT AAT GTG ACT ACC AGA ATT TGG AAC GGG ACT TTC GCA TCA TCA ACC 3264  
 Val Asn Val Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr  
 1045 1050 1055  
 TTC CAG ACA GTA CAG CTA ACG GCA GCT GCA GAA ATC AAC ACC TAT AAC 3312  
 Phe Gln Thr Val Gln Leu Thr Ala Ala Ala Glu Ile Asn Thr Tyr Asn  
 1060 1065 1070 1075  
 CCT GAG ATA TAT GTG ATT GAA GAT AAC ACT GTT ACG ATT CCC CTG ATG 3360  
 Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met  
 1080 1085 1090  
 ATA ATG AAA CCT GAT GAG AAA GCC GAA GTA CCA ACA GAT CCC GAG 3405  
 Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu  
 1095 1100 1105  
 CTGCTGGAAG CAGGCTCAGC GCTCCTGCCT GGACGCATCC CGGCTATGCA GCCCCAGTCC 3465  
 AGGGCAGCAA GGCAGGCCCC GTCTGCCTCT TCACCCGGAG CCTCTGCCCG CCCCCTCAT 3525  
 GCTCAGGGAG AGGGTCTTCT GGCTTTTTTCC CAGGCTCTGG GCAGGCACAG GCTAGGTGCC 3585  
 CCTAACCCAG GCCCTGCACA CAAAGGGGCA GGTGCTGGGC TCAGACCTGC CAAGAGCCAT 3645  
 ATCCGGGAGG ACCCTGCCCC TGACCTAAGC CCACCCCAAA GGCCAAACTC TCCACTCCCT 3705  
 CAGCTCGGAC ACCTTCTCTC CTCCCAGATT CCAGTAACTC CCAATCTTCT CTCTGCA 3762  
 GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA 3807  
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 1110 1115 1120  
 GGTAAGCCAG CCCAGGCCTC GCCCTCCAGC TCAAGGCGGG ACAGGTGCCC TAGAGTAGCC 3867  
 TGCATCCAGG GACAGGCCCC AGCCGGGTGC TGACACGTCC ACCTCCATCT CTTCCTCA 3925  
 GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA 3973  
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 1125 1130 1135  
 CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG 4021  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 1140 1145 1150

GTG GTG GAC GTG ACC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC 4069  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

1155

1160

1165

GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG 4117  
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

1170

1175

1180

1185

CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC 4165  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His

1190

1195

1200

CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA 4213  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

1205

1210

1215

GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA 4255  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

1220

1225

1230

GGTGGGACCC GTGGGGTGCG AGGGCCACAT GGACAGAGGC CGGCTCGGCC CACCCTCTGC 4315  
CCTGAGAGTG ACCGCTGTAC CAACCTCTGT CCTACA GGG CAG CCC CGA GAA CCA 4369  
Gly Gln Pro Arg Glu Pro

1235

CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG 4417  
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln

1240

1245

1250

GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC 4465  
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

1255

1260

1265

GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACC 4513  
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

1270

1275

1280

1285

09155514.1199

CCT CCC GTG CTG GAT TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC 4561  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

1290 1295 1300

ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC 4609  
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

1305 1310 1315

GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC 4657  
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

1320 1325 1330

CTG TCT CCG GGT AAA TGA 4675  
 Leu Ser Pro Gly Lys

1335

Sequence No. 20

Length of sequence: 27

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
 Sequence

GCTCGAGCAA ACCCAGCGCA ACTACGG 27

Sequence No. 21

Length of sequence: 21

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
 Sequence

ATAGTGCCCT GATGACCATT G 21

09155514 11198

Sequence No. 22

Length of sequence: 22

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

GATGGCTTTA ATGATGTGAT TG

22

Sequence No. 23

Length of sequence: 21

Type of sequence: Nucleic acid

Number of strands: Single

Topology: Linear

Kind of sequence: Other nucleic acid, synthetic DNA  
Sequence

TGTTGGTACT TCGGCTTTCT C

21

Sequence No. 24

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Ile Pro Glu Leu Ile Val Cys

1

5

Sequence No. 25

Length of sequence: 8

Type of sequence: Amino acid  
Topology: Circular  
Kind of sequence: Peptide  
Sequence

Cys Met Arg Tyr Thr Ser Ala Cys

1

5

Sequence No. 26

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Glu Trp Met Lys Arg Phe Cys

1

5

Sequence No. 27

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Tyr Thr Thr Arg Leu Lys Cys

1

5

Sequence No. 28

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide



Sequence

Cys Leu Arg Tyr Ser Val Pro Cys

1

5

Sequence No. 29

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Ile Val Asn Arg Leu Gly Cys

1

5

Sequence No. 30

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Gly Leu Gln Ala Leu Pro Cys

1

5

Sequence No. 31

Length of sequence: 8

Type of sequence: Amino acid

Topology: Circular

Kind of sequence: Peptide

Sequence

Cys Lys Leu Lys Gly Thr Met Cys

1

5